



FIG. 1

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1 GGTCTCTGGAGCGCCCTGGGTTGCCCGGCCGGTCCCTGCCGCTGACTTGTTGACACTGCG
61 AGCACTCAGTCCCTCCCGCGCGCCTCCTCCCCGCCCCGCCGCTCCTCCTCCCTGTA
121 ACATGCCATAGTGCGCCTGCGACCACACGGCCGGGGCGCTAGCGTTGCGCTTCAGCCACC
181 ATGGGGAATGGGATGAACAAGATCCTGCCCGGCCTGTACATCGGCAACTTCAAAGATGCC
M G N G M N K I L P G L Y I G N F K D A 20
241 AGAGACGCGGAACAATTGAGCAAGAACAAGGTGACACATATTCTGTCTGTCCATGATAGT
R D A E Q L S K N K V T H I L S V H D S 40
301 GCCAGGCCTATGTTGGAGGGAGTTAAATACCTGTGCATCCCAGCAGCGGATTCAACATCT
A R P M L E G V K Y L C I P A A D S P S 60
361 CAAAACCTGACAAGACATTTCAAAGAAAGTATTAAATTCAATCACGAGTGCCGGCTCCGC
Q N L T R H F K E S I K F I H E C R L R 80
421 GGTGAGAGCTGCCTTGTACACTGCCTGGCCGGGGTCTCCAGGAGCGTGACACTGGTGATC
G E S C L V H C L A G V S R S V T L V I 100
481 GCATACATCATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGCGTGCT
A Y I M T V T D F G W E D A L H T V R A 120
541 GGGAGATCCTGTGCCAACCCCAACGTGGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAAG
G R S C A N P N V G F Q R Q L Q E F E K 140
601 CATGAGGTCCATCAGTATCGGCAGTGGCTGAAGGAAGAATATGGAGAGAGCCCTTTGCAG
H E V H Q Y R Q W L K E E Y G E S P L Q 160
661 GATGCAGAAGAAGCCAAAAACATTCTGGGTAAATATAAGGAGCAAGGGCGCACAGAGCCC
D A E E A K N I L G K Y K E Q G R T E P 180
721 CAGCCCGGCGCCAGGCGGTGGAGCAGTTTTCCGGCACTGGCTCCGCTGACCTACGATAAT
Q P G A R R W S S F P A L A P L T Y D N 200
781 TATACGACGGAGACCTAACGCAAGCGACCTGCTGCCTTCCTTCCCACTGCTTGTCTTCAG
Y T T E T * 205
841 TGTGCCCGGCTGGGCAGGGTGCGGTGGTGGTGGCCGATGAGACAGGAAAGGGAGATAGCC
901 AGGGCGAGGTGGGGCGAGGGCTCTTTCCCCCAAGCAACACCGCCCAGCCTTGTTCCAGGC
961 CCTTGCACTCCGCCCACCCTACCTGGCTGCACCTGAGCTTGCTGCCCCCGGGGATGTTGC
1021 CCAGTGGCTGTGCACTGCTCTGTGCACGTGCGTGTGTGTGAGTGCACTTGTGTGTGGGTG
1081 ACTAAGTGGATGCATGTGTGTGCCTGTGTGAGTGAGGGTATGTGCACCTAAGTGTGTACA
1141 TGTGTGTATGTTGTGAAAGTGTCTGTGCACATGAATGTTGTGTGAGTGTGAACTCTTTC
1201 TTACTGCTGGAAGTCACA 1218

FIG.2

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1  AGCCCCGGCGCGGCCATGGGGAGTGGGATGAGCCAGATCCTGCCGGGCCTGTACATTGGCA
    M G S G M S Q I L P G L Y I G N 16
61  ACTTCAAAGACGCAAGAGATGCAGAACAGTTGAGCAGGAACAAGGTGACACACATTCTTT
    F K D A R D A E Q L S R N K V T H I L S 36
121  CTGTGCACGATACTGCCAGGCCCATGTTGGAGGGAGTTAAATACCTGTGTATTCCAGCGG
    V H D T A R P M L E G V K Y L C I P A A 56
181  CAGACACACCATCTCAAACCTGACAAGACATTTCAAAGAAAGCATTAAATTCATTCATG
    D T P S Q N L T R H F K E S I K F I H E 76
241  AGTGCCGACTCCAGGGTGAGAGCTGTCTGTACATTGCCTGGCTGGGGTCTCCAGGAGTG
    C R L Q G E S C L V H C L A G V S R S V 96
301  TGACATTGGTGATCGCATACATCACGACTGTCACCGACTTTGGCTGGGAAGATGCCTTGC
    T L V I A Y I T T V T D F G W E D A L H 116
361  ACACTGTTTCGTGCGGGAGGTCCTGTGCCAACCCCAACCTGGGCTTTCAAAGGCAGCCGC
    T V R A G R S C A N P N L G F Q R Q P Q 136
421  AGGAGTTTGAGAAACATGAAGTGACCAAGTATCGGCAATGGCTGAGAGAAGAGTATGGAG
    E F E K H E V H Q Y R Q W L R E E Y G E 156
481  AGAACCCCTTTGCGGGATGCAGAAGAAGCCAAAATATTCTGGGTAAATATAAAGAGCAAG
    N P L R D A E E A K N I L G K Y K E Q G 176
541  GGCGCATGGAGCCCCGGCCTAGCAGCAGGCGGTGGAGCAGCTTCTCAACCTGCCTCCTC
    R M E P R P S S R R W S S F S T L P P L 196
601  TCACCTACAATAACTACACAACAGAGACCTAACAGAGAGAGCTGGTGTCTGCCTTCCTGC
    T Y N N Y T T E T * 205
661  TGCGGGTCTTCTGGGTTGCCTACCATGTGCTGGTGTGCCTGGTGTGCTGGCTCCTGCCTC
721  TGAGGACTACGAGAGGAGGTGCGCAGCAAGGTGGAGCACTCAGGGCTCCTTCTCAGAATAC
781  CGCCCTACTCAGGCTTTTTCACTCTCCCATCTTCGCCCCATCTTTTCTCACCTGAACCT
841  GCCCCAACCTGGGATGCTGCCCGGCCACCGTGTACTTCTCGTATGTGTGCAGGCGTGTGGA
901  TGTGCATGTATGTGTCTAAGAGTGTGCATATATACCTACAAATGTATGCATTGTGAACAA
961  GTACACATGTAAATGTGTCTCTGCATGTGGGCACTGAGTGTATGGTGTGCTGAAAGTTAT
1021  AAACACCCGCTGCCAGAAGTCAATGGTCAATCCCACATGGAAGTCATTTG
1081  AACTTGCCCTCCTGGAAGCTACTCCACCAAGTACAGCTTATGCCTGTGCTGAGTGAGAG
1141  CTCAGGGTGTGGGACAGCTGGAACAGTGGTGTTCAGATTCTGAGATGGCACAGAGGAAG
1201  GGACAGGACCCTCCTGAGGAAGAGTGGCATAATCCTAGTGAGTTTTATGTCTGTGGGAAC
1261  AAGGGAGGGGCTTTCTGAGCACTGTCTTGACTTGATAAGTATACTTGCCAGCCCGTCAT
1321  GGCCCTGAGTTCACCTGGTGCCTGCTCTGCGTGGGACCAGCGTCATTTGACTTTCATGGT
1381  GATATGGTATGGTGACAGGGTGGACCTGAGACTCAGTAGGCCTATACCAGAGGCTGGCC
1441  CACTCCTGTCTGCTTTTAAACACTTTAGCTCTGGCTTAGCTCTTGTGACGGGCTCAT
1501  CTCAGGTTTGCATGTACCTGCAGGAAGTGGAAAGAAAGGCAGTTATTAACCTCCATAGCC
1561  ATTTGTGATTTAAATGCCTACGCATTCACTGAGCTCACTGTTGTATGCTGTGGATTGA
1621  CCGCTACCTCATGAAGTTCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT
1681  TCCTTCCTTTCTTTCTTTCTTTAAGGTTGAGGTTTCTTTGGTACCCAGTCAACTCTGCTT
1741  CATAGTTGAGAAATGTTTGTATGTGACTATTGTTTTTGAACCAAAGAGAAGAGCATACT
1801  TATGTCATTGAGTGATTTAAATTTGACGTTTGGCTTGGCTTCTGTAGGGTTTCTAGTGCA
1861  AACCTACATTCTGACCATGAGAGTCTTATGTTCAAAGTATGTGGCAGCAGGCACCCCTAG
1921  AAGTTTTGCACAGTCCAGTGTCCAGTCTTTTATGCCAATTACGTTGCTTAAGCATGCAG
1981  GACCATGCAAATGAAAATACACTCAACCTCTCCCTAAACGTAAGTGTGACAGGCATCTC
2041  TGAAGCTTAAGAAACCCCAAGAAGCCCCGAGGAGCTGGACAGTGGTGGCACACACCTT
2101  TAATCCCAGCTTTTGGGAGGCAGAGGCAGGCGGATTTCTGAGTTCAAGGCCAGCCTGGTC
2161  TACAGAGTGAGTTCAGGACAGCCAGGGCTACACAGAGAAACCCGTGTCGAAACCAA
2221  AAAAAAAAAAAAAAAAAAAGGAGAAGCCCTGAGGAAGAAGCAGCAGGCTCTCTCTGTGT
2281  GTGTGGAGCTCTCAGGGACCCAGGGAAGGTGTGGTTGCCAGCTCTCTGTGTGACGGCCGT
2341  GCCAAGCAATAGCATGAGTGACGCTGAGTACCTGAGTATGTGTGCACGTGTATGAACAG
2401  CTGCATACCTTTCCATAGGTTCTCAACTGTCTCAATTTTTGTTGCCAGTAATGTTCTTTC
2461  FCCACAGCTGCTCCGGGAATTCTGAAGTACTGGGCCTTTCTCAGAAGACTGTAATGTACC
2521  TGAAGTTTCTGAAATATTGCAAAGTTTCAGGCTGGTGCTGCCAAAAGAAAGTGTATGTA
2581  AGTTTATTTTAAAGAAATCCAATAGTGATTTGTATACTTGTTTTTTTTCATTTTAAACCA
2641  AATGCATGTATAATCATGTGGGAATATGTTAAGATCTATGGATATTCTGTAGCAAGAGAA
2701  ATATCTTTGCCTTAACTCCACTGCTGTGGTTGTTTCTTGGACCTGACCGATGCTCATACA
2761  ATAATCTCAAGAGCCCTGTCTGTTTCGTAATAGTAACTACTTCTCATGAACACTACCCAA
2821  GGAGGAAGCCTGCACCTGGGAAGTGTGCAGTGTGAGCTCTGCCCTCCTGTAAAGTTCTCC
2881  AGCTCTAGACATGTCTCTGGGTGTGTTTTATCTACTGGTGTATTCTATATGGTATGAA
2941  TTACCAAAGCTATTTCAGATTTCTTAATAAAGGGCAAATCCCGGAATCTTTGNTTTTTA
3001  CCCTGGAAGA 3010

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FIG. 3(a)

mJKAP MSQILPGLYIIGNF[KD]ARDA[EQ]LSRNK[V]T[H]L[SV]HDTARPMLE--[G-V][KY]LC[IP]AA[DT]PSQN[L]TRHF

pucker ed ASP [W]F[P]H[L]L[LG]NGR[D]ADNPSSVGA--NC[VL]NVT[C]Q[S]PNESH[LQ][G-L][KY]MQ[IP]AS[DT]PHQ[N]KQ[YF]
 rMKP3 [PVE]ILP[F]LYLGC[AK]DSTNL[DV]LEEF[GI]KYIILNVT[P]M[L]PNL[F]ENA[G]EF[KY]KQ[IP]IS[DT]HWSQ[N]LSQ[FF]
 rMKPX [PVQ]ILP[Y]LYLGC[AK]DSTNL[DV]LGKY[GI]KYIILNVT[P]M[L]PNL[F]ENA[G]EF[TY]KQ[IP]IS[DT]HWSQ[N]LSQ[FF]
 hMKP4 [PVQ]ILP[N]LYLGS[AR]D[SAN]LES[LA]KL[GI]RYIILNVT[P]M[L]PNL[F]ENA[G]EF[HY]KQ[IP]IS[DT]HWSQ[N]LSR[FF]
 rMKP2 [PVE]ILP[F]LYLGS[AY]H[AAR]D[M]LDAL[GI]TAL[LI]NVSS[DC]PNHFE--[G]HYQY[KC]IPVE[DN]HKA[DT]SS[WF]
 mMKP1 [PVE]ILS[F]LYLGS[AY]H[ASR]K[D]M[L]DAL[GI]TAL[LI]NVSS[DC]PNHFE--[G]HYQY[KC]IPVE[DN]HKA[DT]SS[WF]
 mM3/6 LTR [ILP]H[L]LYLGS[QK]D[VLN]K[D]L[M]TQNG[IS]YV[L]N[AS]NSC[PK]PDFIC-ES[RE]MR[IP]INDNYCEK[L]P[WL]
 mPAC1 [PVE]ILP[Y]LYLGS[CN]HSSD[LQ]G[AC]G[IT]AL[V]LNV[S]ASCP[N]HFE--[G]LFHY[KC]IPVE[DN]QMV[ET]SA[WF]
 hVH3 [PVE]ILP[F]LYLGS[AY]H[ASK]C[EF]LAN[H]U[TA]LLNV[S]RR[T]SEAC-M-THL[HY]KWI[PVE]DSHTA[DT]IS[SHF]
 hVHR VGNASVAQD [IP]K[LQ]KLGIT[HV]LNAEGRS[F]M[H]VNT[AN]F[K]YK-DS[G-I]TYL[GI]KAN[DT]QE[F]NLSA[YF]

...c.o.d.s.e.n.s.u.s.....r.v..i.l.p.f.l.v.l.g.s.a.k.d.....d.v.l.....g.i.t..i.l.o.v.t..n..p.o..f.....g..f.k.y.k...l.p.i..D.....n.l.s..f.f

[K]E[S]I[K]F[I]H-E[CR]LQGESCLVHCL[AGV]SR[S]V[TLV]IAY[I]T[V]TDFGWED[AL]H[T]V[RA]GRSCAN[P]N[L]G[F]Q[R]O[P]Q[E]F[E]K[H]E

QEAY[F]I[E]-DARRK[TS]R[V]L[H]CH[AG]ISRS[AT]IAIAY[V]MRYK[S]L[S]L[E]AY[K]L[V]KVAR[P]IISPN[L]NFMGQ[L]L[E]EQNL
 PEATISFID-EARRGKNCGVLVHCL[AG]ISRS[V]T[V]TAYL[M]QK[L]NLS[M]NDAY[D]I[V]K[M]K[S]N[IS]PNF[N]FMGQ[L]L[D]FERTL
 PEATISFID-EARRSKKCGVLVHCL[AG]ISRS[V]T[V]TAYL[M]QK[L]NLS[M]NDAY[D]I[V]K[M]K[S]N[IS]PNF[N]FMGQ[L]L[D]FERTL
 PEATISFID-EALSQNCGLVHCL[AG]ISRS[V]T[V]TAYL[M]QK[L]HLS[L]NDAY[D]I[V]K[M]K[S]N[IS]PNF[N]FMGQ[L]L[D]FERTL
 MEATISFID-AV[K]DCRGR[V]L[V]HCL[AG]ISRS[AT]ICL[AY]L[M]RTNR[V]K[L]DEAF[E]FV[K]Q[R]R[S]IISPNF[S]FMGQ[L]L[Q]FESQV
 NEATISFID-SI[K]DAGGR[V]E[V]HCL[AG]ISRS[AT]ICL[AY]L[M]RTNR[V]K[L]DEAF[E]FV[K]Q[R]R[S]IISPNF[S]FMGQ[L]L[Q]FESQV
 DKSI[E]FID-KAKLSSCCQV[V]VHCL[AG]ISRS[AT]IAIAY[I]MKT[M]GMS[D]D[AY]R[F]V[K]D[R]R[P]SISPNF[N]GQ[L]L[E]YERSL
 QEATISFID-SVKNSSGG[V]L[V]HCL[AG]ISRS[AT]ICL[AY]L[I]QSHR[V]LDEAF[D]FV[K]Q[R]R[S]IISPNF[S]FMGQ[L]L[Q]FESQV
 QEATISFID-CVREKGG[V]L[V]HCL[AG]ISRS[PT]ICMAYL[M]KTKQFR[L]KEAF[D]YI[K]Q[R]R[S]M[V]SPN[F]GFMGQ[L]L[Q]VESEI
 ERAA[F]IDQALAQKNG[V]L[V]HCL[AG]ISRS[PT]LVIAYL[M]MRQK[M]DV[K]S[AL]SIV[R]QNR-EIGPN[DG]F[A]Q[L]CQLNDR[L]

...e.a.i.e.f.i.d.....f.....r.v.j.v.h.c..a.g.i.s.r.s..i.i..v.a.y.i.m.....j..l..d.a.y.d.f.y.k..k.r.s..i.s.p.n.f..f.m.g.q.i.l.d.f.e.....j

FIG.3(b)

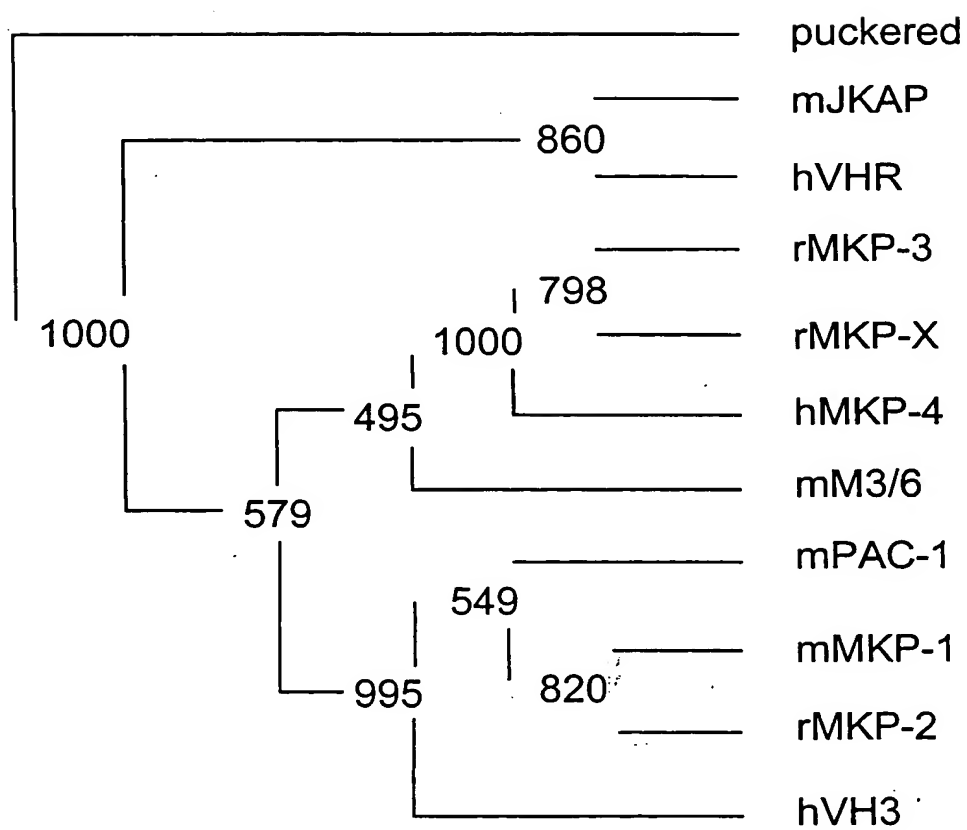


FIG.3(c)

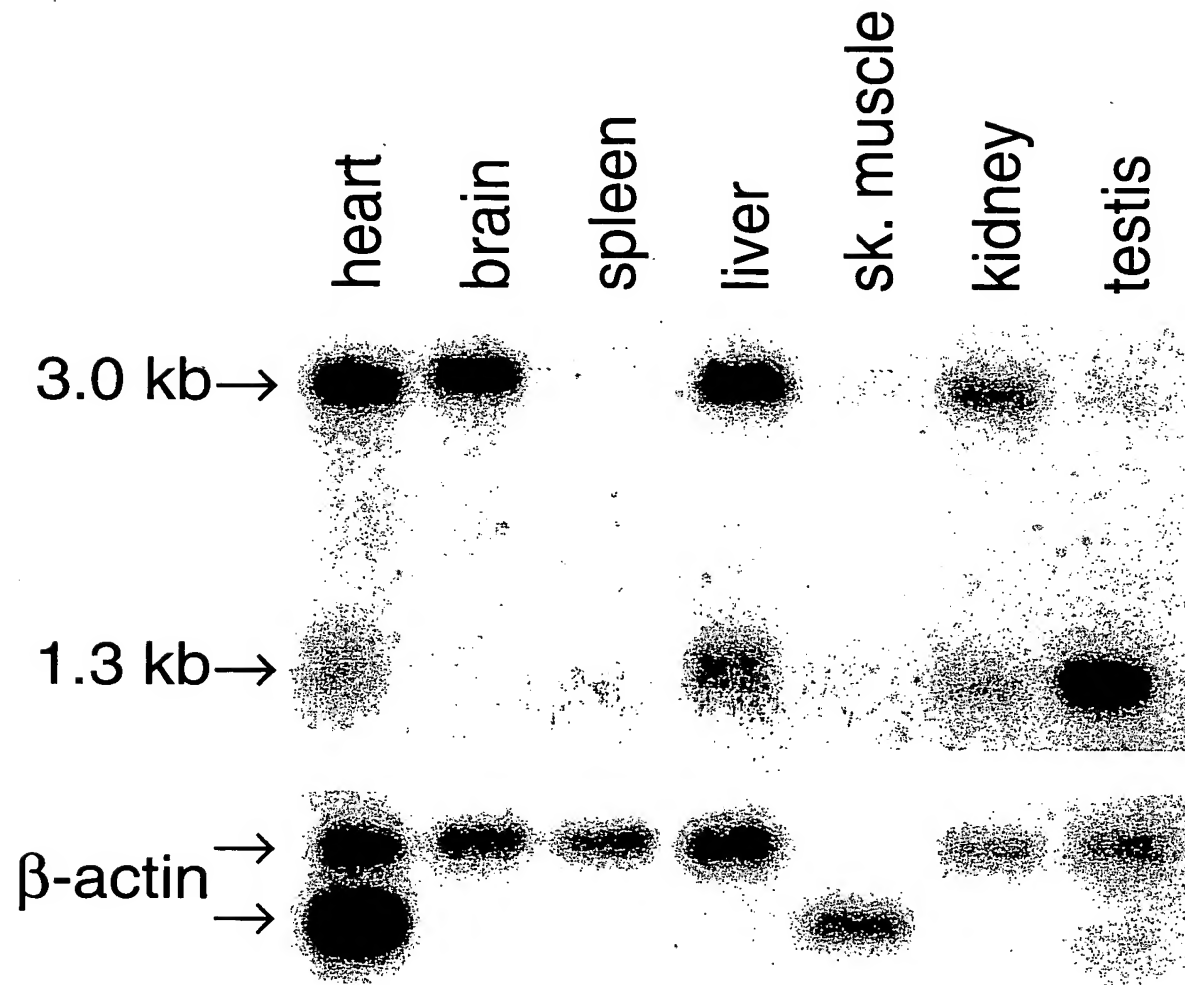
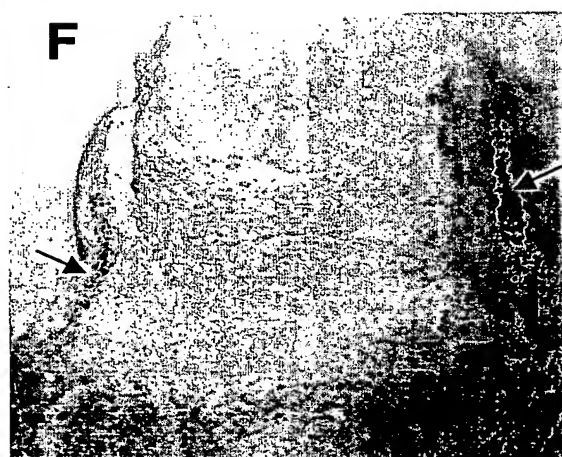
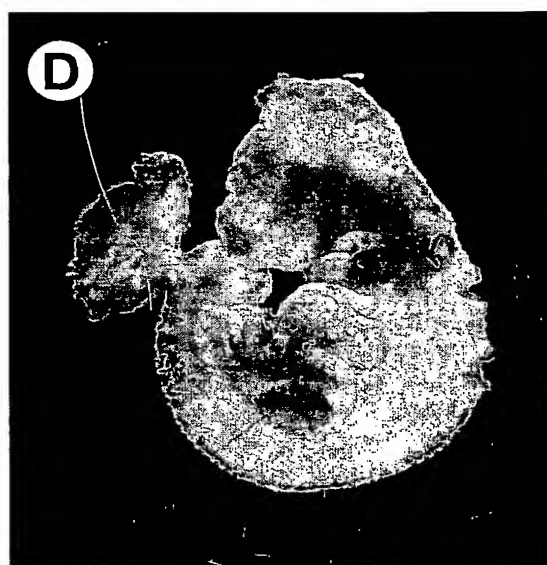
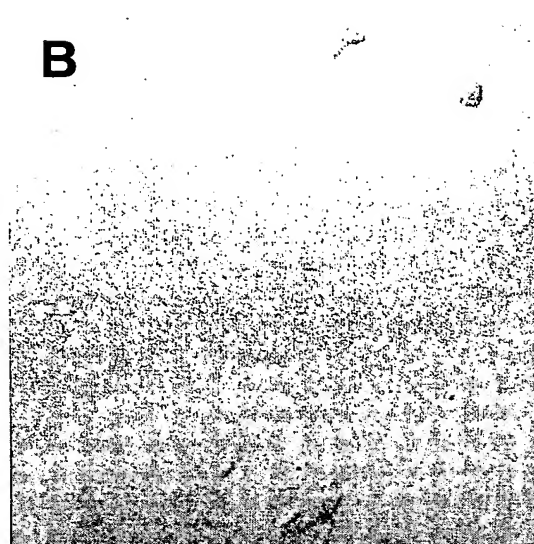
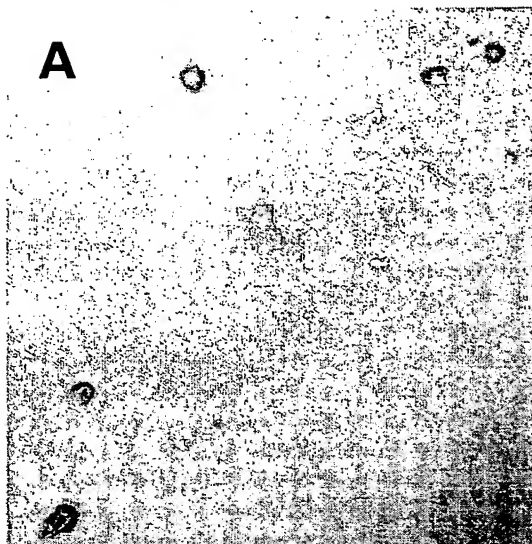
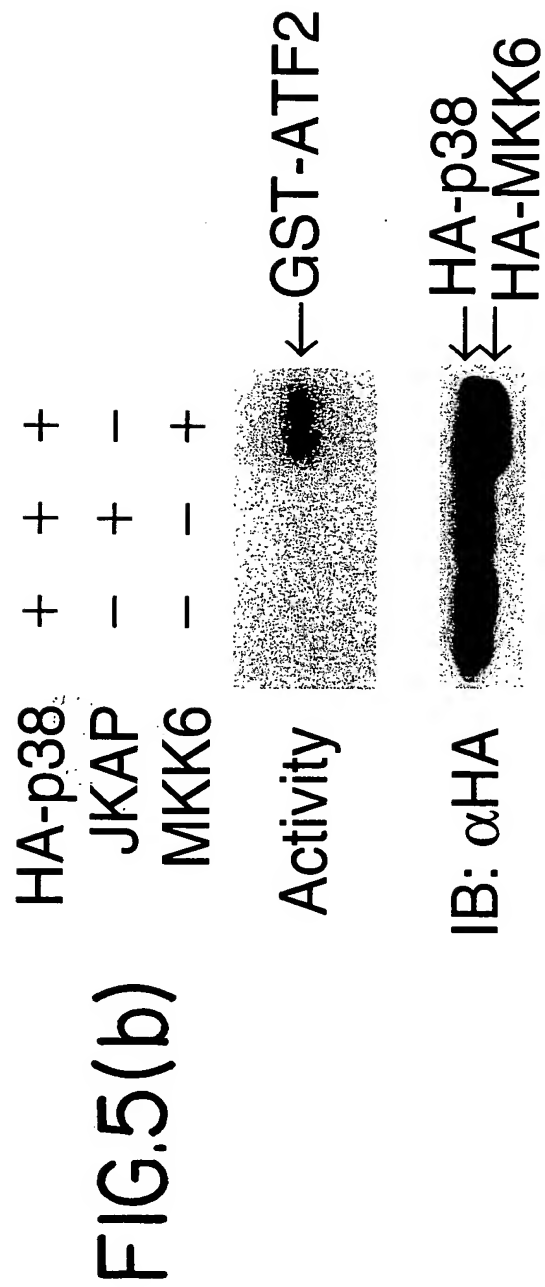
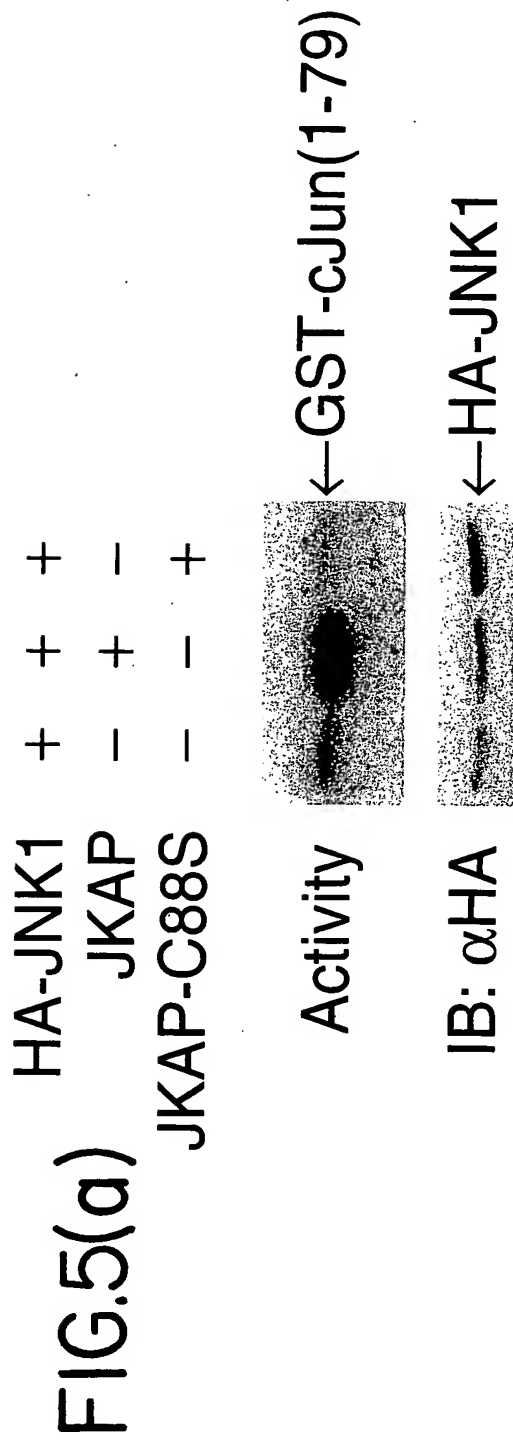


FIG.4

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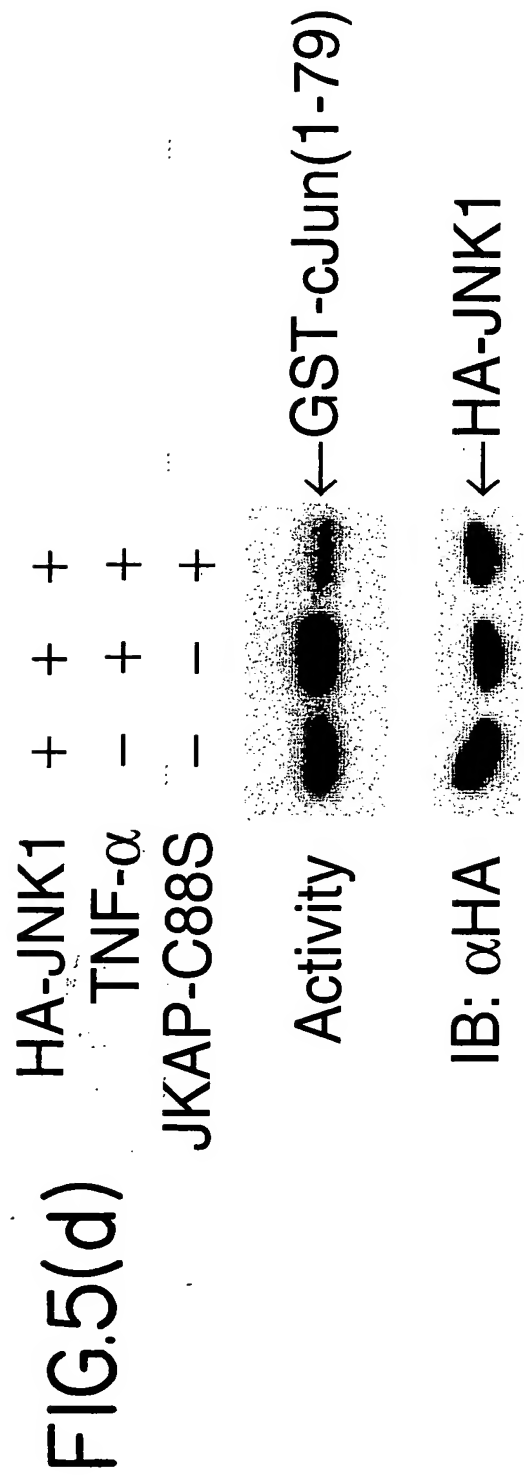
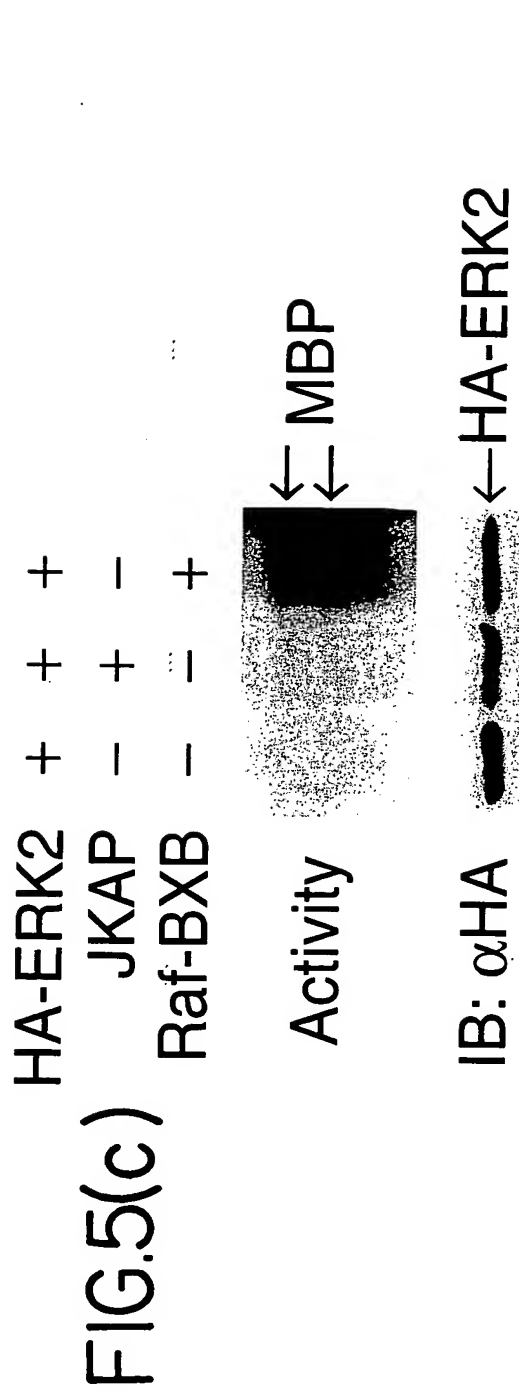
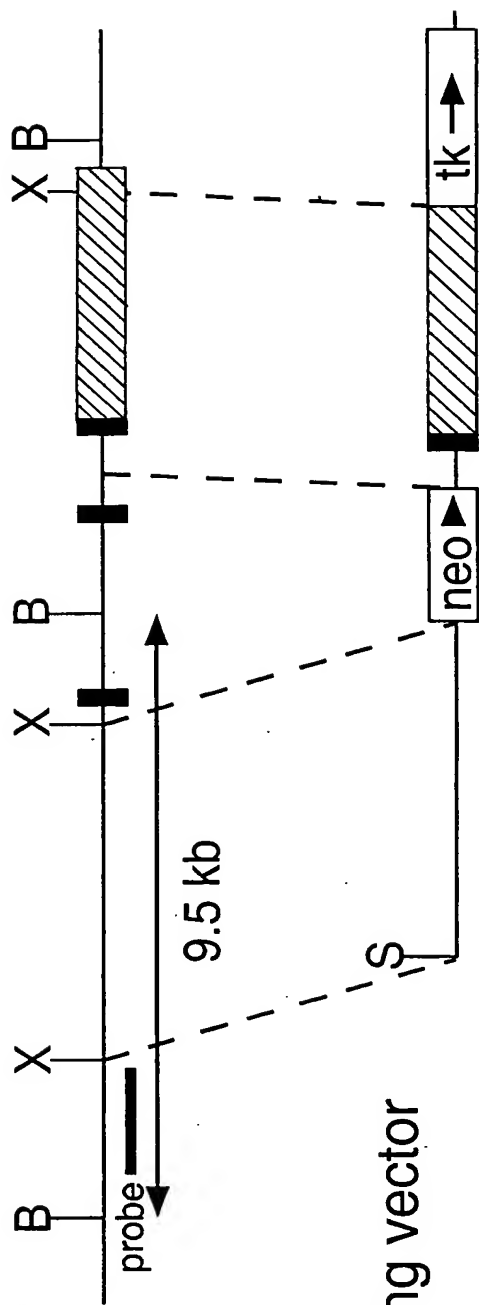


FIG.6(a)

Jkap locus



Targeting vector

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Homologous recombination

Mutated *Jkap* locus

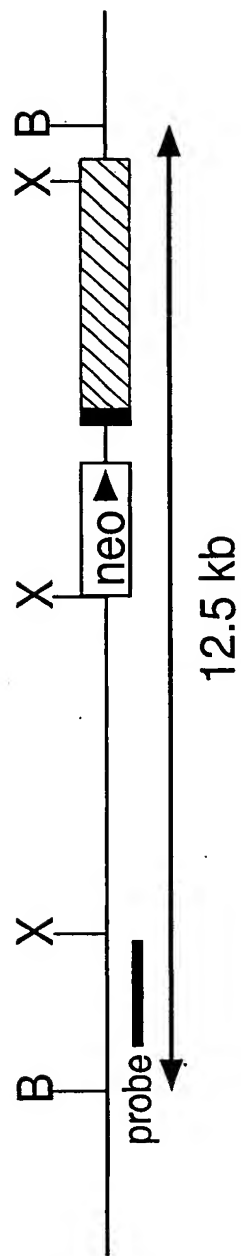


FIG.6(b)

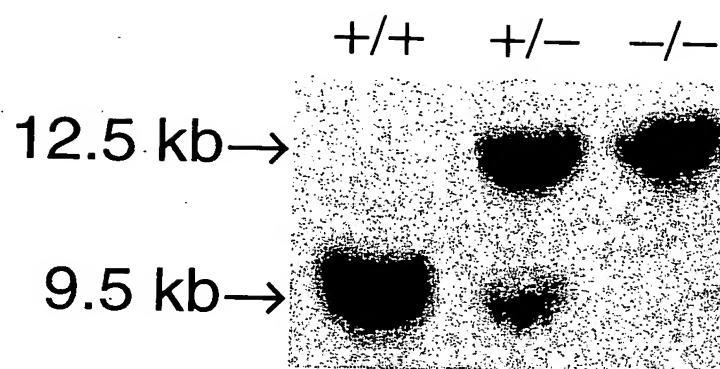


FIG.6(c)

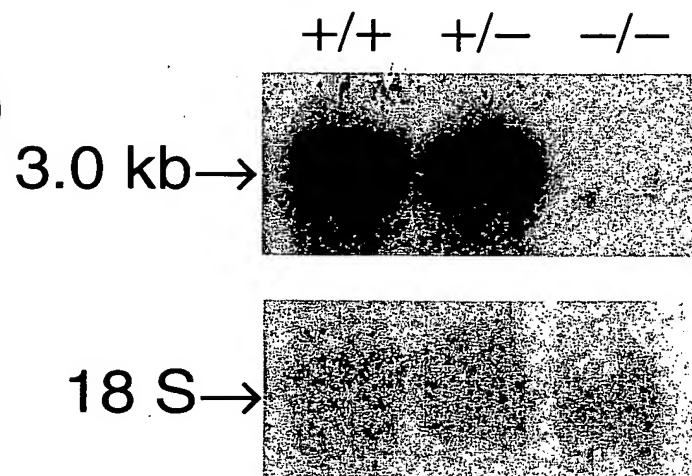


FIG.7(a)

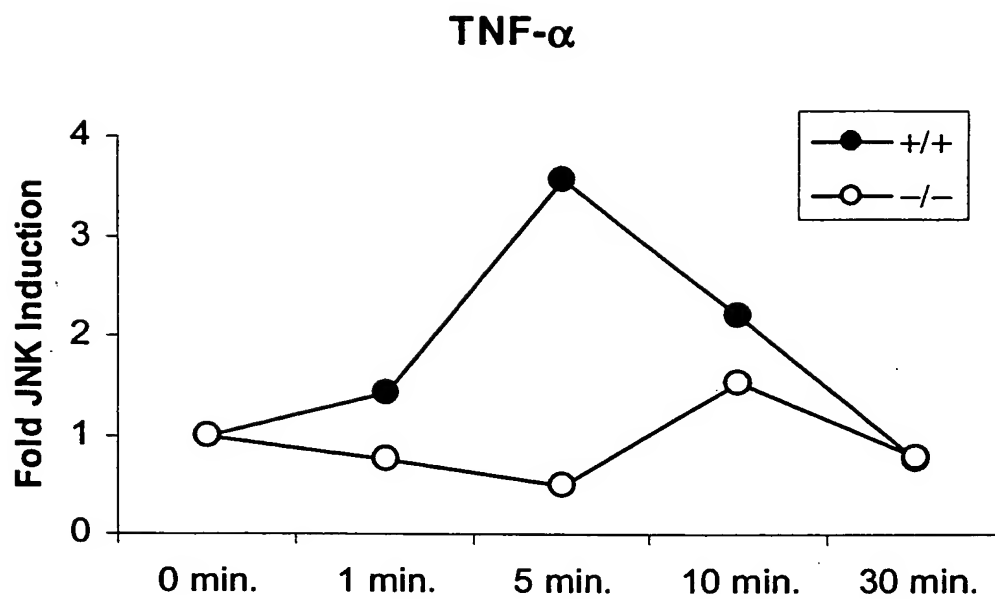


FIG.7(b)

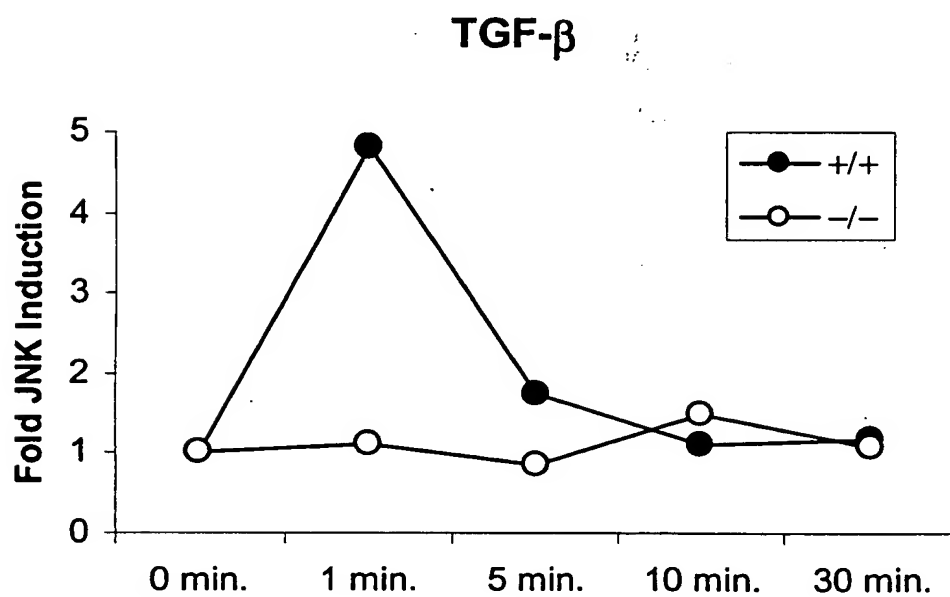


FIG.7(c)

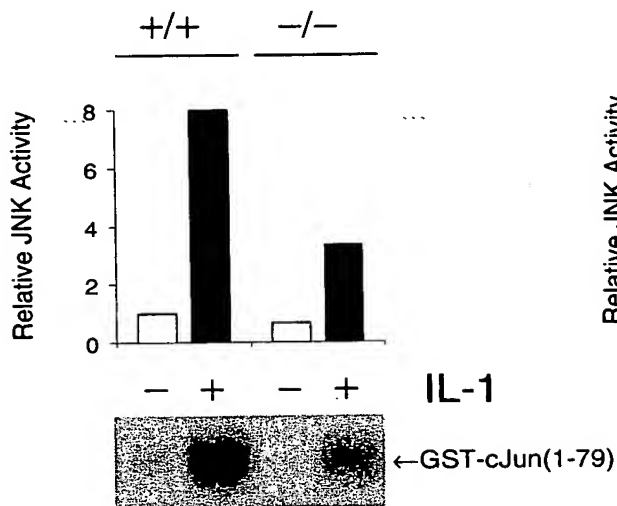


FIG.7(d)

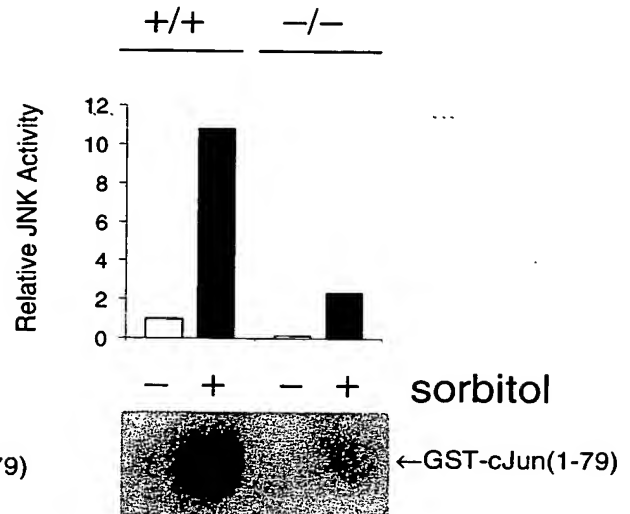


FIG.7(e)

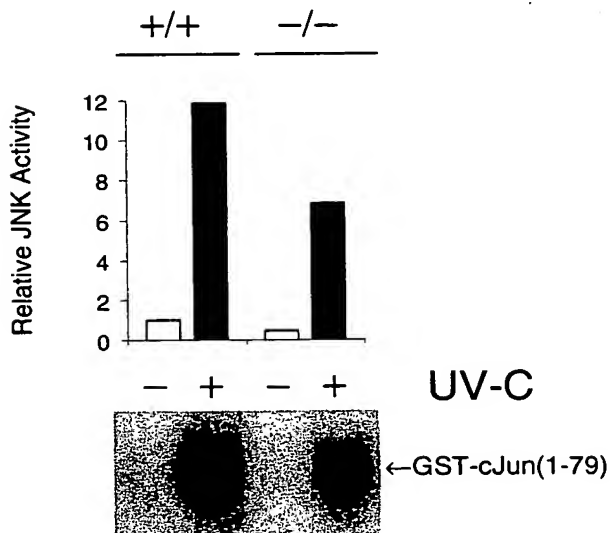


FIG.7(f)

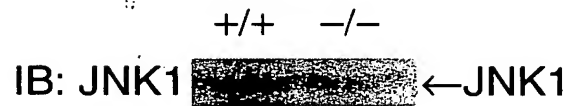


FIG.7(g)

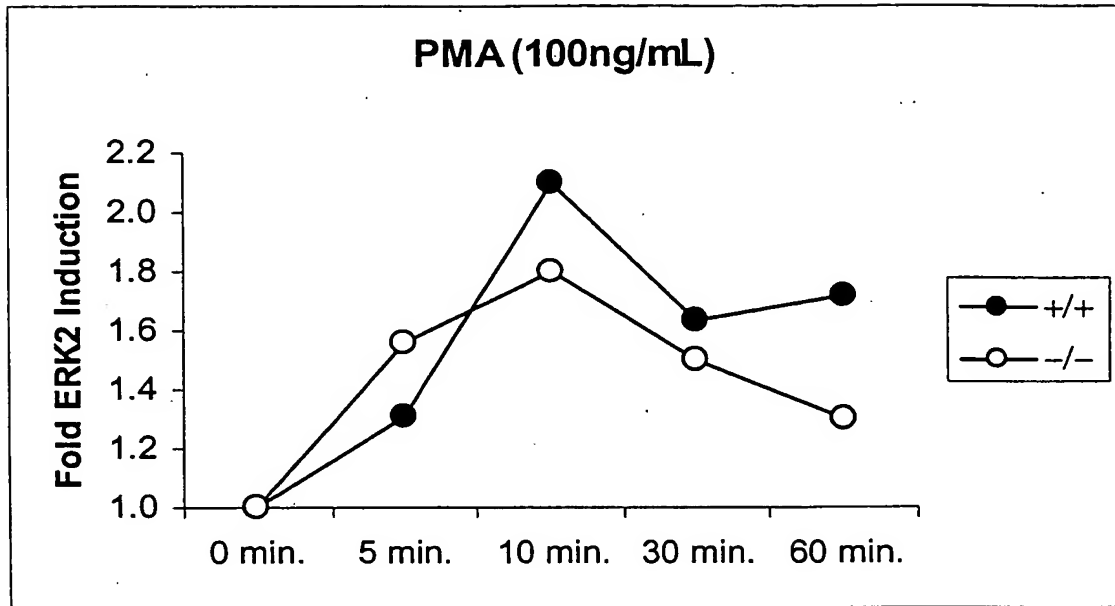
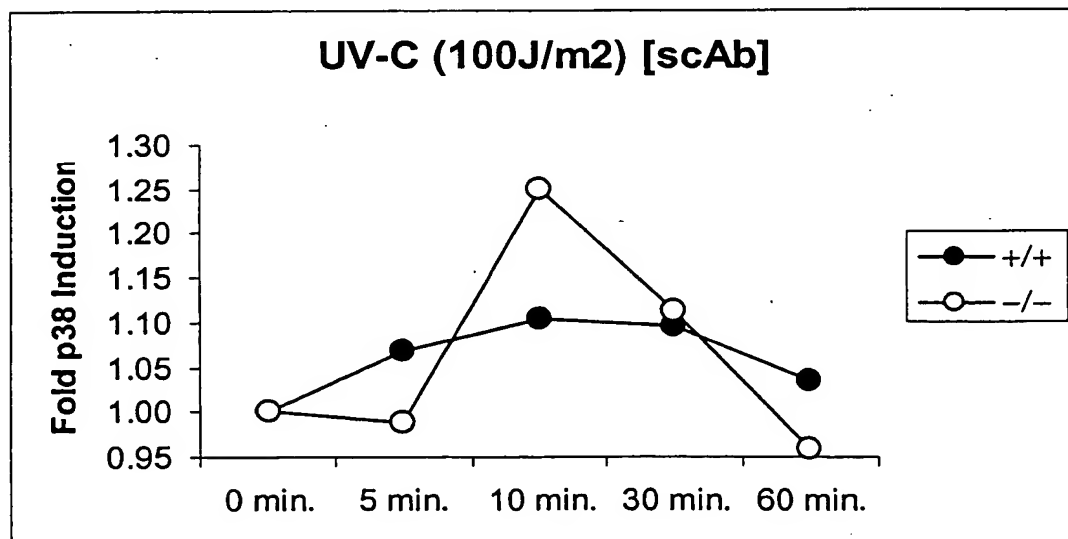


FIG.7(h)



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FIG.8(a)

HPK1	-	+	+
<i>myc</i> -JKAP	-	-	+

IP: α HPK1IB: α *myc*← *myc*-JKAPIB: α HPK1

← HPK1

FIG.8(b)

JKAP	-	-	+
HPK-1	-	+	+
HA-JNK1	+	+	+

Activity



← GST-cJun(1-79)

FIG. 8(c)

